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GenCore version 5.1.6
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                 Copyright
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- protein search, using sw model OM protein November 12, 2003, 15:41:34; Search time 9.84282 Seconds (without alignments) 640.499 Million cell updates/sec Run on:

Title: Perfect score:

US-09-963-347B-2 769 1 MGCPRMFPFALLYVLSVSFR......KKRRKRKTTTNKCLEQVSQL 149

Sequence:

Scoring table:

328717 segs, 42310858 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

328717 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% .

Maximum Match 100%
Listing first 45 summaries

Issued Database :

Patents AA:\*

/cgm2\_6/ptodata/2/iaa/5A\_COMB.pep:\*
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/cgm2\_6/ptodata/2/iaa/6A\_COMB.pep:\*
/cgm2\_6/ptodata/2/iaa/6B\_COMB.pep:\*
/cgm2\_6/ptodata/2/iaa/PTTUS\_COMB.pep:\*
/cgm2\_6/ptodata/2/iaa/PTTUS\_COMB.pep:\* .........

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 2. Appli	4			Sequence 2, Appli	·ψ	7	7	Sequence 2, Appli	574		46,	4,	46,	46	4	46,	46,	53,	Sequence 53, Appl	53,	23	23	23	53	4,	Sequence 9, Appli
SUMMARIES	ID	US-09-852-391-2	US-09-328-352-6455	US-08-993-228-10	US-09-627-986-1	US-09-213-053-2	US-09-417-485D-6	80-	US-08-231-205A-2	US-08-871-161-2	US-09-328-352-5747	US-08-286-889-46	US-08-485-618-46	US-08-362-652-46	US-08-605-672-46	US-08-482-293A-46	US-08-943-363-46	US-09-193-043-46	US-09-688-307A-46	US-08-485-618-53	US-08-362-652-53	US-08-605-672-53	US-08-482-293A-53	US-08-943-363-53	US-09-193-043-53	US-09-688-307A-53	US-09-356-952-4	US-08-430-286A-9
	DB	4	4	0	4	æ	4,	Н	Н	N	41	Н	ч	н	(1	N	N	m	4	Н	Н	N	7	7	m	4	m	m
	Query Match Length	159	674	1461	465	1394	2184	154	154	154	667	1155	1155	1155	1155	1155	1155	1155	1155	1161	1161	1161	1161	1161	1161	1161	1589	440
ok	Query	91.9	10.6	9.5	•	6.3		9.5	9.5	9.5	9.5	9.1	9.1	9.1	9.1	9.1	9.1	9.1	9.7	9.1	9.1	6.	6	9.1	9.1	9.1	•	œ
	Score	707	81.5	73	72.5	71.5	71.5	71	71	71	71	70	70	10	70	70	70	70	70	70	70	70	70	70	70	70	69	89
	Result No.	1	71	m	4	IJ.	9	7	œ	ወ	10	11	12	13	14	15	16	17	18	513	20	21	22	23	24	72	26	27

Sequence 2, Appli	Sequence 317, App		Sequence 21, Appl	21.	Ч	14.	Sequence 12, Appl	14,	12.	М	9	Sequence 6, Appli	10,	2	10,	10.	10,
US-09-308-375-2	US-09-198-452A-317	US-09-252-991A-27368	US-07-937-609-21	US-08-029-170-21	US-08-220-151-12	US-08-220-151-14	US-08-413-118-12	US-08-413-118-14	US-08-473-446-12	US-08-473-446-14	US-09-213-053-6	PCT-US92-00282-6	US-08-430-286A-10	US-07-725-083-2	US-08-669-286-10	US-09-469-253-10	US-09-642-146-10
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2285	354	154	411	411	459	459	459	459	459	459	459	531	451	782	782	782	782
8.8	8.8	8.7	8.7	8.7	8.7	8.7	8.7	8.7	8.7	8.7	8.7	8.6	8,6	9.8	8.6	8.6	8.6
68	67.5	63	63	67	67	67	67	67	67	67	67	66.5	99	99	99	99	99
28	53	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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TEFNNIVSCSNRPHCLIEIQSLTFNPNRRVRSLAKEMFAMKTKAALAIWCPGYSETQINA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 TEFINITYSCSNRPHCLTEIQSLTFNPTAGCASLAKEMFAMKTKAALAIWCPGYSETQINA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MFPFALLYVLSVSFRKIFILQLVGLVLTYDFTNCDFEKIKAAYLSTISKDLITYMSGTKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 MFPFALLYVLSVSFRKIFILQLVGLVLTYDFTNCDFEKIKAAYLSTISKDLITYMSGTKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 707; DB 4; Length 159;
Pred. No. 2.5e-75;
); Mismatches 5; Indels
                                  Sequence 2. Application US/09852391

Batent No. 655520

GENERAL INFORMATION:
APPLICANT: Sims, John
APPLICANT: Lyman, Stewart
APPLICANT: Lyman, Stewart
APPLICANT: Mastrong, Allison
APPLICANT: Human TSLP DNA and Polypeptides
FILE REFERENCE: 03260.0087-00304/2881-WO
CURRENT APPLICATION NUMBER: US/09/852,391
CURRENT FILING DATE: 2001-05-09
PRIOR APPLICATION NUMBER: 60/108,452
PRIOR APPLICATION NUMBER: 60/108,452
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PATENT Ver. 2.0
SEQ ID NO 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               91.9%; Score ... 36.5%; Pred. No. 2.5e-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126 TOAMKKRRKKVTTNKCLEOVSOL 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 96.5
Matches 139; Conservative
                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 159
TYPE: PRT
ORGANISM: Homo sapiens
RESULT 1
US-09-852-391-2
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65 9

> 121 g

RESULT 2
US-09-328-352-6455
US-09-328-352-6455

Sequence 6455, Application US/09328352

Patent No. 6562958

GENERAL INFORMATION:

APPLICANT: Gary L. Breton et al.

TILLE OF INVENTION: BULGAIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

TILLE OF INVENTION: BAUGANII FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC99-03PA

CURRENT APPLICATION NUMBER: US/09/328,352

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GenCore version 5.1.6

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OM nucleic - nucleic search, using sw model

Run on:

November 12, 2003, 15:45:54; Search time 56 Seconds

(without alignments)

3783.284 Million cell updates/sec

Title:

Perfect score: 480

Sequence:

1 atgstcccttttgccttact......ctttactgaaacaacagtaa 480

Scoring table:

Gapop 10.0, Gapext 1.0

Searched:

569978 segs, 220691566 residues

Total number of hits satisfying chosen parameters:

139956
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Issued Patents NA:\*

| Issued Patents NA:\*
| Cgn2 6/ptodata/2/ina/5A COMB.seq:\*
| Cgn2 6/ptodata/2/ina/6A COMB.seq:\*
| Cgn2 6/ptodata/2/ina/6A COMB.seq:\*
| Cgn2 6/ptodata/2/ina/BCOMB.seq:\*
| Cgn2 6/ptodata/2/ina/PCTUS COMB.seq:\*
| Cgn2 6/ptodata/2/ina/PCTUS COMB.seq:\*
| Cgn2 6/ptodata/2/ina/PCTUS COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	Sequence 1, Appli	<u>ب</u> ه	Sequence 1, Appli		42	524,	Sequence 1, Appli	Sequence 1, Appli	1456	Sequence 2, Appli	Sequence 1, Appli	Sequence 321, App	Sequence 5, Appli	10,	4.	ហ	'n	را س	Sequence 1, Appli	٦		Sequence 153, App	412,			114,	1, Ap
SUMMAKIES	ID	US-09-852-391-1	US-09-198-452A-1	US-08-916-421B-1	PCT-US94-09752-2	US-09-288-143-42	US-09-328-352-524	US-09-557-884-1	US-09-643-990A-1	US-09-252-991A-14566	US-09-103-840A-2	US-09-103-840A-1	US-09-404-879A-321	US-08-026-145-5	US-08-446-646-10	US-08-446-646-4	US-08-817-707-5	US-09-734-675-3	US-08-916-421B-1	US-09-557-884-1	US-09-643-990A-1	US-07-885-089B-5	US-08-858-207A-153	US-09-671-317-412	US-09-481-049-6	US-09-356-806-112	US-09-356-806-114	US-08-697-954-1
	08	4	4	4	Ŋ	4,	4	4	4	4	m	ო	4	Н	Н	н	m	4	4	4	4	ď	4	4	4	4	4	m
	Length DB	743	1230025	1664976	1881	1734	2460	1830121	1830121	1218	4403765	4411529	069	231	234	450	2373	38844	1664976	1830121	1830121	866	1282	1001	1073	1976	2312	3212
640	Query Match	100.0	7.2	7.0	9.9	6.5		6.5	6.5	6.3	6.3	6.3	6.3	6.2	6.2	6.2	6.2	6.2	6.2	6.2	6.2	6.1	6.1	6.1	6.1	6.1	6.1	6.1
	Score	480	34.4	33.4	31.8	31	31	31	31	30.4	30.4	30.4	30.2	30	30	30	29.6	29.6	29.6	29.6	29.6	29.4	29.4	29.5	29.5	29.3		29.5
	Result No.	1		o O		in U		7	80	σ	c 10	c 11	12	13	14	15	16	c 17	18	Н	c 20	C	22	23	24	25	26	27

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                                    Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 1003, Ap
Sequence 1, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 CAACTTGTAGGGCTGGTGTTAACTTACGACTTCACTAACTGTGACTTTGAGAAAGATTAAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        260 CAACTIGIAGGGCTGGTGTAACTTACGACTTCACTAACTGTGACTTTGAGAAGATTAAA 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 GCAGCCTATCTCAGTACTATTTCTAAAGACCTGATTACATATATGAGTGGGACCAAAAGT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          320 GCAGCCTATCTCAGTACTATTCTAAAGACCTGATTACATATATGAGTGGGACCAAAAGT 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               380 ACCGAGTTCAACAACACGTCTCTTGTAGCAATCGGCCACATTGCCTTACTGAAATCCAG 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 AGCCTAACCTTCAATCCCACCGCCGCTGCGTCGCTCGCCAAGGAAATGTTCGCCATG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 ACCGAGTTCAACAACACCGTCTCTTGTAGCAATCGGCCACATTGCCTTACTGAAATCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTPPGGGTTACTATGTTCTGTCAGTTTCTTTCAGGAAAATCTTCATCTTA
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  Sequence 1, 7
Sequence 3, 7
Sequence 3, 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09852391
Patent No. 655528
GENERAL INPORMATION:
APPLICANT: Lyman, Stewart
APPLICANT: Lyman, Stewart
APPLICANT: Armstrong, Allison
APPLICANT: ONSERING: 00326.0087-00304/2881-WO
CURRENT FILING DATE: 2004-05-09
PRIOR APPLICATION NUMBER: 60/108,452
PRIOR APPLICATION NUMBER: 60/108,452
PRIOR APPLICATION NUMBER: 60/108,452
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 480; DB 4; L
100.0%; Pred No. 2.9e-148;
tive 0; Mismatches 0;
US-08-545-528D-1

US-09-183-245-3

US-09-183-245-3

US-09-727-169-3

US-09-727-168-3

US-09-726-968-3

US-09-134-011C-1003

US-09-134-011C-1003

US-09-137-169-1

US-09-127-169-1

US-09-727-169-1

US-09-727-169-1

US-09-727-169-1

US-09-727-169-1

US-09-727-169-1

US-09-727-169-1
                                                                                                                                                                                   US-09-429-093-1
US-08-913-374-1
US-09-012-669F-2
US-08-084-718-64
                                                                                                                                                                                                                                                                 ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 480; Conservative
               TYPE: DNA
ORGANISM: Homo sapiens
US-09-852-391-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
  SEQ ID NO 1
LENGTH: 743
                                                                                                                                                                                                                                                                                                      RESULT 1
US-09-852-391-1
  0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
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OTHER INFORMATION: n=a or or g or t
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LOCATION: (450001)...(465000)
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NAME/KEY: misc feature
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NAME/KEY: misc feature
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NAME/KEY: misc feature
LOCATION: (36001)..(37500)
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OTHER INFORMATION: n=a or c or g or
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LOCATION: (525001)..(540000)
OTHER INFORMATION: n=a or c or g or
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OTHER INFORMATION: n=a or c or g
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LOCATION: (510001)..(525000)
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LOCATION: (495001)..(510000)
OTHER INFORMATION: n=a or c or g
                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/09198452A

Sequence 1, Application US/09198452A

GENERAL INFORMATION:
APPLICANT: Griffais, R.
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prever TITLE OF INVENTION: and treatment of infection
TITLE OF INVENTION: and treatment of infection
CURRENT APPLICATION NUMBER: US/09/198,452A

CURRENT FILING DATE: 1998-11-24

SEQ ID NO: 6849

SEQ ID NO: LENGTH: 1230025
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LOCATION: (210001)..(225000)
OTHER INFORMATION: n=a or c or g or t
COTHER INFORMATION: n=a or c or g or t
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LOCATION: (30001)..(45000)

NAME/KEY: misc feature
LOCATION: (30001)..(45000)

NAME/KEY: misc feature
LOCATION: (45001)..(60000)

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OTHER INFORMATION: n=a or c or g or t
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LOCATION: (75001)..(90000)

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NAME/KEY: misc feature
LOCATION: (105001)..(120000)

OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (105001)..(120000)
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LOCATION: (120001)..(135000)
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LOCATION: (135001)...(150000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (150001)...(165000)
OTHER INFORMATION: n=a or c or g or t
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LOCATION: (16501)..(180000)
OTHER INFORMATION: n=a or c or g or
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OTHER INFORMATION: n=a or c or g or make/KEY: misc feature
LOCATION: (15001)...(3000)
OTHER INFORMATION: n=a or c or g
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ORGANISM: Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                             RESULT 2
US-09-198-452A-1/c
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November 12, 2003, 15:41:34; Search time 10.5034 Seconds (without alignments) 640.499 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                        328717 segs, 42310858 residues
                                                                                                   OM protein - protein search, using sw model
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. 1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*
5: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*
6: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued\_Patents AA:\*

Database :

	Description	Sequence 2, Appli	645	4	46,	46,	46,	46,	46,	46,	46,	53,	53,	53	23	53	53	23	10	41.	ø	N	7	7	Sequence 7, Appli	4	7	273
SUMMARIES	ID	US-09-852-391-2	US-09-328-352-6455	-88	US-08-485-618-46	US-08-362-652-46	US-08-605-672-46	US-08-482-293A-46	US-08-943-363-46	US-09-193-043-46	US-09-688-307A-46	US-08-485-618-53	-652-5	US-08-605-672-53	US-08-482-293A-53	US-08-943-363-53	US-09-193-043-53	US-09-688-307A-53	US-08-993-228-10	US-09-198-452A-415	PCT-US92-00282-6	US-08-949-588-2	US-09-213-053-2	US-09-627-986-1	US-09-180-827-7	US-09-356-952-4	US-09-308-375-2	US-09-252-991A-27368
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	Score	823	74.5	73	73	73	73	73	73	73	73	73	73	73	73	73	73	73	73	71	69.5	69.5	69.5	68.5	68	89	69	67
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US-09-328-352-4934	7-4-0-6/3-00-60	US-09-115-824-2	US-08-975~762-53	US-09-295-028-53	US-09-106-582-53	US-09-328-352-5747	US-09-170-496D-292	US-08-746-111-5	US-08-946-026-4	US-08-948-276-4	US-08-344-695-2	US-08-446-908-2	US-08-231-205A-2	US-08-871-161-2	US-08-361-920-25	US-08-479-939-25	US-08-483-432-25
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ALIGNMENTS

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1 MPPFALLYVLSVSFRKIFILQLVGLVLTYDFTNCDFEKIKAAYLSTISKDLITYMSGTKS 60
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                                                                                    APPLICANT: Lyman, Stewart
APPLICANT: Lyman, Stewart
APPLICANT: Lyman, Stewart
APPLICANT: Armstrong, Julison
APPLICANT: Armstrong, Hilary
TITLE OF INVENTION: Human TSLP DNA and Polypeptides
FILE REFERENCE: 03260.0087-00304/2881-WO
CURRENT APPLICATION NUMBER: US/09/852,391
CURRENT FILING DATE: 2001-05-09
PRIOR APPLICATION NUMBER: 60/108,452
PRIOR APPLICATION NUMBER: 60/108,452
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.0
                     Sequence 2, Application US/09852391; Patent No. 6555520; GENERAL INFORMATION:
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Best Local Similarity 100.0
Matches 159; Conservative
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US-09-852-391-2
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US-09-852-391-2
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61 TEFNNTVSCSNRPHCLTEIQSLTFNPTAGCASLAKEMFAMKTKAALAIWCPGYSETQINA 120 61 TEFNNIVSCSNRPHCLTEIQSLIFNPTAGCASLAKEMFAMKTKAALAIWCPGYSETQINA 120 121 TQAMKKRRKKVTTNKCLEQVSQLQGLWRRFNRPLLKQQ 159 121 TOAMKKRRKKVTTNKCLEQVSQLQGLWRRFNRPLLKQQ 159 RESULT 2 US-09-328-352-6455 d ð ద

Sequence 6455, Application US/09328352
Retent No. 6562958
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLETC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BUMMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352

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(without alignments)
640.499 Million cell updates/sec
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2: /cgn2_6/ptodata/2/laa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/laa/6A_COMB.pep:*
7: /cgn2_6/ptodata/2/laa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/laa/RCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/laa/RCTUS_COMB.pep:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	,	Appli	Appl	Appl	App1	App1	App1	Appl	App1	Appl	App1	Appl	App1	Appl	Appl	Appl	Appl	Appl	Appli	Appli	Appl:	App1	App1	Appl	Appli	Appli	2736B, A	Annli
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	Description	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Secretarion
SUMMAKIES	ID	US-09-852-391-2	US-08-286-889-46	US-08-485-618-46	US-08-362-652-46	US-08-605-672-46	US-08-482-293A-46	US-08-943-363-46	US-09-193-043-46	US-09-688-307A-46	US+08-485-618-53	US-08-362-652-53	US-08-605-672-53	US-08-482-293A-53	US-08-943-363-53	US-09-193-043-53	US-09-688-307A-53	US-08-993-228-10	PCT-US92-00282-6	US-09-356-952-4	US-09-308-375-2	US-08-975-762-53	US-09-295-028-53	US-09-106-582-53	US-08-948-276-4	US-09-627-986-1	US-09-252-991A-27368	TIS-07-668-648-6
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c	% Query Match	100.0	10.8	10.8	10.8	10.8	10,8	10.8	10.8	10.8	•		10.8	10.8	10.8	10.8	10.8	10.8	10.3	10.1	9.9	9.8	9.8	9.8	9.7	7.6	9.6	9
	Score	675	73	73	73	73	73	73	73	73	73	73	73	73	73	73	73	73	69.5	68	67	99	99	99	65.5	'n	65	i,
	Result No.	1	7	m	4,	2	9	7	ω	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24		56	27

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Sequence 505, App
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Sequence 46, Application US/08286889
Petent No. 5470953
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Mich
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTYON: No. 5470953el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
                                 Sequence 6,
Sequence 2,
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         Seguence
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APPLICANT: Lyman, Stewart
APPLICANT: Lyman, Stewart
APPLICANT: Armstrong, Jalison
APPLICANT: Hillison
APPLICANT: Hillison
APPLICANT: Armstrong, Hillison
APPLICANT: 103260.0087-00304/2881-WO
FILE REFERENCE: 03260.0087-00304/2881-WO
CURRENT APPLICATION NUMBER: US/09/852,391
CURRENT FILING DATE: 2001.05-09
PRIOR APPLICATION NUMBER: 60/108,452
PRIOR APPLICATION NUMBER: 60/108,452
NUMBER OF ERQ ID NOS: 5
SOSTWARE: Patentin Ver. 2.0
                                                                               PCT US91_0231_6
US-09-107-532A-4455
US-09-101-470-4
US-09-066-046-29
US-09-066-047-15
US-09-066-047-15
US-08-029-170-17
PCT_US92_02091_2
US-09-138-452A-121
US-09-198-452A-121
US-09-044-225-2
US-09-044-245-2
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US-08-429-998-6
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Best Local Similarity 100.
Matches 131; Conservative
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US-08-286-889-46
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